

**Figure 1 – Human STR\_50E1 – SEQ ID NO:1**Nucleotide sequence of long splice variant

[initiation ATG and stop codons are underlined]

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GGGCTCCCTG CACAAATGCG TTGGGTGATG GGGGCTGAAT CCAGCCCACA CTGCACTTGC CAAGCCAGCT 70
GGGGCCCTGG CACAAGACAG TCCCAGCCTG TTTTCACTGA CTTTGCTAAT TCTCACGGAG GCACCATGTG 140
GTGTGGGAAG GCCCGGTCTT CGTAACCTCT CTGCTCCCAG GTCCCTGACC AGTCCTTAAC ACACAGTGGT 210
CTTTGCTCAC CTGCGGCCCA GCTCTGGGCT CTCCCCAAG CATCCTTTGC CTTGCCTCCC TCCCATCTTC 280
CTCTGGGCCT TCTCTCTGCT CCTGCCAGG AAAGTGTGCT CTCAGGAGCG CAGGAGCCAG CTCTCAGCCC 350
CCATCTCCTG GGCACCTACC GTACTCAGGA AATATGTTCT GAATTCAGGA TTATCCTCAT TCTACTGAGA 420
AGACCTGGAG GACAGAAATC AGCAAGACCT AAAGGGGAGA GGAAGGAGGG CCAGGCTGGG GTGGAGGTGC 490
CCCACCCGGG AGCCCGGGCG CAGCCTCACC GCAGGCTGAT TCACAGAAGG CTCAGAGGGT TGCGAGGGCC 560
CAATCGGCAC TGTCATCTG CCCAGGCTCT GAGTCACCAG CTGGTGAGGG GCAGCTGCAG CCCAGCAGGA 630
AACAAAGTCT AGCATGGAAG AGGTGGGAGG GAGGTGGTGG GGCCTGAAAC CCCGCTGGC TGGCCTTAGA 700
GGAAGTGGGA GTGACTGTCC GGCACCTGCT CAGCAGCAA CAGCTCTCAA GGACGTGCTA GGAGTCAGGA 770
ACTGGGCCAG CTCCGGTCCC TTCCTTTTGG GGCTCTCACT CTGGAGGATG GGGTGGATGG GAGGTCAGAG 840
GAGCACCAGC CTATGGCCCT GGACACCTGG GGTATTCAGC GAGTTCCTGG AGGACGGTGG GATGGGGCTG 910
TGTTCCAGC AAGAAAAAAC CGGAAGATC CTGACGGAGT TCCTCCAGTT CTATGAAGAC CAGTATGGCG 980
TGCTCTCTT CAACAGCATG CGCCATGAGA TTGAGGGCAC GGGGCTGCCG CAGGCCAGC TGCTCTGGCG 1050
CAAGGTGCCA CTGGACGAGC GCATCGTCTT CTCGGGGAAC CTCTCCAGC ACCAGGAGGA CAGCAAGAAG 1120
TGGAGAAACC GCTTCAGCCT CGTGCCCCAC AACTACGGG TGGTGCTCTA CGAAAACAA GCGGCCTATG 1190
AGCGGCAGGT CCCACCAGA GCGTCATCA ACAGTGCAGG CTACAAAATC CTCACGTCCG TGAACCAATA 1260
CCTGGAGCTC ATTGGCAACT CCTTACCAGG GACCACGGCA AAGTCGGGCA GTGCCCCCAT CCTCAAGTGC 1330
CCCACACAGT TCCCCTCAT CCTCTGGCAT CCTTATGCGC GTCACCTACTA CTTCTGCATG ATGACAGAAG 1400
CCGAGCAGGA CAAGTGGCAG GCTGTGCTGC AGGACTGCAT CCGGCACTGC AACAAATGAA TCCCTGAGGA 1470
CTCCAAGTA GAGGGCCCTG CGTTCACAGA TGCCATCCGC ATGTACCGAC AGTCCAAGGA GCTGTACGGC 1540
ACCTGGGAGA TGCTGTGTGG GAACGAGGTG CAGATCCTGA GCAACCTGGT GATGGAGGAG CTGGGCCCTG 1610
AGCTGAAGGC AGAGCTCGGC CCGCGGCTGA AGGGGAAACC GCAGGAGCGG CAGCGGCAGT GGATCCAGAT 1680
CTCGGACGCC GTGTACCACA TGGTGACGA GCAGGCCAAG GCGCGCTTCG AGGAGGTGCT GTCCAAGGTG 1750
CAGCAGGTGC AGCCGGCCAT GCAGGCCGTC ATCCGAAGTG ACATGGACCA AATTATCACC TCCAAGGAGC 1820
ACCTTGCCAG CAAGATCCGA GCCTTCATCC TCCCCAAGGC AGAGGTGTGC GTGCGGAACC ATGTCCAGCC 1890
CTACATCCCA TCCATCCTGG AGGCCCTGAT GGTCCCCACC AGCCAGGGCT TCACTGAGGT GCGAGATGTC 1960
TTCTTCAAGG AGGTCACGGA CATGAACCTG AACGTATCA ACGAGGGCGG CATTGACAAG CTGGGCGAGT 2030

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ACATGGAGAA GCTGTCCCGG CTGGCGTACC ACCCCCTGAA GATGCAGAGC TGCTATGAGA AGATGGAGTC 2100  
 GCTGCGACTG GACGGGCTGC AGCAGCGATT TGATGTGTCC AGCACGTCCG TGTTCAGCA GCGAGCCCAG 2170  
 ATCCACATGC GGGAGCAAAT GGACAATGCC GTGTATACGT TCGAGACCCT CCTGCACCAG GAGCTGGGGA 2240  
 AGGGGCCCCAC CAAGGAGGAG CTGTGCAAGT CCATCCAGCG GGTCTGAGAG CGGGTGCTGA AAAAATACGA 2310  
 CTACGACAGC AGCTCTGTGC GGAAGAGGTT CTTCCGGGAG GCGCTGCTGC AGATCAGCAT CCCGTTCTCTG 2380  
 CTCAAGAAGC TGGCCCCCTAC CTGCAAGTCG GAGCTGCCCC GGTTCAGGA GCTGATCTTC GAGGACTTTG 2450  
 CCAGGTTTCAT CCTGGTGGAA AACACGTACG AGGAGGTGGT GCTGCAGACC GTCATGAAGG ACATCCTGCA 2520  
 GGCTGTGAAG GAGGCCGCGG TGCAAGGAA GCACAACCTC TACCGGGACA GCATGGTCAT GCACAACAGC 2590  
 GACCCCAACC TGCACTGCT GGGCGAGGGC GCGCCCATCG ACTGGGGCGA GGAGTACAGC AACAGCGGGC 2660  
 GGGGCGGCGAG CCCCAGCCCC AGCACCCCGG AGTCAGCCAC CCTCTCGGAA AAGCGACGGC GCGCCAAGCA 2730  
 GGTGGTCTCT GTGGTCCAGG ATGAGGAGGT GGGGCTGCC TTTGAGGCTA GCCCTGAGTC ACCACCACCT 2800  
 GCGTCCCCCG ACGGTGTCAC TGAGATCCGA GGCCTGCTGG CCCAAGGTCT GCGGCCTGAG AGCCCCCAGC 2870  
 CAGCCGGCCC CCTGCTCAAC GGGGCCCCCG CTGGGGAGAG TCCCCAGCCT AAGGCCGCCC CCGAGGCCCTC 2940  
 CTCGCCGCT GCCTCACCCC TCCAGCATCT CTGCGCTGGA AAGGCTGTGG ACCTTGGGCC CCCCAGCCCC 3010  
 AGCGACCAGG AGACTGGAGA GCAGGTGTCC AGCCCCAGCA GCCACCCCGC CCTCCACACC ACCACCGAGG 3080  
 ACAGTGCAGG GGTGCAGACT GAGTTCTAGG CCAGTGGGTC CCTGACTGCT GCACATGGCA GAGGCCGTTT 3150  
 CCTTCCGGAC CCAGGCAGGC TCAGCTCTGG GGAGGGCACC CTGGTCTGTG CCTTGTGGGT GGAGGCGGGG 3220  
 CAGGGCTGTG TGCACCGCC AGGGAGCGGG CCCACCTGAG TCACTTTATT GGGTTCAGTC AACACTTTCT 3290  
 TGCTCCCTGT TTTCTCTTCT GTGGGATGAT CTCAGATGCA GGGGCTGGTT TTGGGGTTTT CCTGCTTGTG 3360  
 CCAAGGGCTG GACACTGCTG GGGGGCTGGA AAGCCCTCC CTTCTGTCC TTCTGTGGCC TCCATCCCCT 3430  
 CATGGGTGCT GCCATCCTTC CTGGAGAGAG GGAGGTGAAA GCTGGTGTGA GCCAGTGGG TTCCCGCCCA 3500  
 CTCACCCAGG AGCTGGCTGG GCCAGGACCG GGAGAGGGAG CACTGCTGCC CTCCTGGCCC TGCTCCTTCC 3570  
 GCAGTTAGGG GTGGACCGAG CCTCGCTTTC CCCACTGTTC TGGAGGGAAG GGAAGGAGG GGGTCTTACG 3640  
 GCTGGAGCCA GCCTGGGGGT GCTGGGTGGA GAGATGAGAT TTAGGGGGTG CCTCATGGG TGGGCAGGCC 3710  
 TGGGGTGAAA TGAGAAAGGC CCAGAACGTG CAGGTCTGCG GAGGGGAAGT GTCCTGAGTG AAGGAGGGGA 3780  
 CCCCATCCTG GGGATGCTGG GAGTGAGTGA GTGAGATGGC TGAGTGAGGG TTATGGGGAG CCTGAGGTTT 3850  
 TATGGGCCTG TGATCCCCT TCTCCCGGCC CCAGCCTGCC TCCCTCCTGC CCGCTGGCC CACAGGTCTC 3920  
 CCTCTGGTCC CTGTCCCTCT GGTGGTTGGG GATGGAGCGG CAGCAAGGGG TGTAATGGGG CTGGGTTCTG 3990  
 TCTTCTACAG GCCACCCCGA GGTCTCAGT GGTTCCTGG GAGCCGGAC GGGGCTCCTG AGGGGTACAG 4060  
 GTTGGGTGGG CCCTCCCTGA GGTCTGGGG TCAGGCTTTG GCCTCTGCTG CCTCTCAGT ACCAAGTCAC 4130  
 CTCCTCTGA AAATCCAGTC CCTTCTTTGG ATGTCCTTGT GAGTCACTCT GGGCTGGCT GTCGTCCCTC 4200  
 CTCAGCTTCT TGTCCTGGG ACAAGGTCA AGCCAGGATG GGGCAGGCN TGGGATCCCC CACCCAGGA 4270  
 CCCCACAGGC CCCCTCCCCT GNTGNTTTCG GGGGGCAGG GCAGAAATGG ACTCCTTTTG GTCCCCGAG 4340  
 GTGGGGTCCC CTCCAGCCC TGCATCCTCC GTGCCCTAGA CCTGCTCCCC AGAGGAGGGG CCTTGACCCA 4410

CAGGAAGTGT GGTGGCGCCT GGCAATCAGG GACCCCCAGC TGCCGCAGCC CTGGTTTTTG GCGCATCTTT 4480  
TCCCTCTTGT CCCGAAGATT TGCGCCTTTA GTGCCTTTTG AGGGGTTCCTC ATCATCCCTC CCTGATATTG 4550  
TATTGAAAAT ATTATGCACA CTGTTTCATGC TTTACTAAT CAATAACGC TTTATTTAAA AAAAAAAAAA 4620  
AAA 4623

**Figure 2 – Human STR\_50E1 – SEQ ID NO:2**Predicted polypeptide of long splice variant

(Alternatively-spliced exon is marked)

MEEVGGRWWG LKPRLAGLRG TGSDCPALAQ QQTALKDVLG VRNWASSGPF LLGLSLWRMG WMG**QQRSTSL** 70  
**WPWTPGVFSE FLEDGGMGLW FQQ**EKTGKIL TEFLQFYEDQ YGVALFNSMR HEIEGTGLPQ AQLLWRKVPL 140  
 DERIVFSGNL FQHQEDSKKW RNRFSLVPHN YGLVLYENKA AYERQVPPRA VINSAGYKIL TSVDQYLELI 210  
 GNSLPGTTAK SGSAPILKCP TQFPLILWHP YARHYFMM TEAEQDKWQA VLQDCIRHCN NGIPEDSKVE 280  
 GPAFTDAIRM YRQSKELYGT WEMLCGNEVQ ILSNLVMEEL GPELKAELGP RLKGGKQERQ RQWIQISDAV 350  
 YHMVYEQAKA RFEEVLISKVQ QVQPAMQAVI RTDMDQIITS KEHLASKIRA FILPKAEVCV RNHVQPYIPS 420  
 ILEALMVPTS QGFTEVRDVF FKEVTDMLN VINEGGIDKL GEYMEKLSRL AYHPLKMQSC YEKMESLRD 490  
 GLQORFDVSS TSVFKQRAQI HMREQMDNAV YTFETLLHQE LGKGPTKEEL CKSIQRVLER VLKKYDYDSS 560  
 SVRKRFREA LLQISIPFL KKLAPTCKSE LPRFQELIFE DFARFILVEN TYEEVVLQTV MKDILQAVKE 630  
 AAVQRKHNLV RDSMVMHNSD PNLHLLAEGA PIDWGEYSN SGGGGSPSPS TPESATLSEK RRRAKQVSV 700  
 VQDEEVGLPF EASPESPPA SPDGVTEIRG LLAQGLRPES PPPAGPLLNG APAGESPQPK AAPEASSPPA 770  
 SPLQHLLPGK AVDLGPPKPS DQETGEQVSS PSSHPALHTT TEDSAGVQTE F 821.

**Figure 3 – Human STR\_50E1 – SEQ ID NO:3**Nucleotide sequence of short splice variant

(Initiation ATG and stop codons are underlined)

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GGGCTCCCTG CACAATGCG TTGGGTGATG GGGGCTGAAT CCAGCCCACA CTGCACTTGC CAAGCCAGCT 70
GGGGCCCTGG CACAAGACAG TCCCAGCCTG TTTTCACTGA CTTTGCTAAT TCTCACGGAG GCACCATGTG 140
GTGTGGGAAG GCCCGGTCTT CGTAACCTCT CTGCTCCCAG GTCCCTGACC AGTCCTTAAC ACACAGTGGT 210
CTTTGCTCAC CTGCGGCCCA GCTCTGGGCT CTCCCCACAG CATCCTTTGC CTGCGCTCCC TCCCATCTTC 280
CTCTGGGCCT TCTCTCTGCT CCTGCCCAGG AAAGTGTGCT CTCAGGAGCG CAGGAGCCAG CTCTCAGCCC 350
CCATCTCCTG GGCACTCACC GTACTCAGGA AATATGTTCT GAATTCAGGA TTATCCTCAT TCTACTGAGA 420
AGACCTGGAG GACAGAAATC AGCAAGACCT AAAGGGGAGA GGAAGGAGGG CCAGGCTGGG GTGGAGGTGC 490
CCCACCCGGG AGCCCGGGCG CAGCCTCACC GCAGGCTGAT TCACAGAAGG CTCAGAGGGT TGGGAGGGCC 560
CAATCGGCAC TGTATCCTG CCCAGGCTCT GAGTCACCAG CTGGTGAGGG GCAGCTGCAG CCCAGCAGGA 630
AACAAAGTCT AGCATGGAAG AGGTGGGAGG GAGGTGGTGG GGCCTGAAAC CCCGCCTGGC TGGCCTTAGA 700
GGAAGTGGGA GTGACTGTCC GGCACCTGGT CAGCAGCAAA CAGCTCTCAA GGACGTGCTA GGAGTCAGGA 770
ACTGGGCCAG CTCCGGTCCC TTCTTTTGG GGCTCTCACT CTGGAGGATG GGGTGGATGG GAGAAAAAAC 840
CGGGAAGATC CTGACGGAGT TCCTCCAGTT CTATGAAGAC CAGTATGGCG TGGCTCTCTT CAACAGCATG 910
CGCCATGAGA TTGAGGGCAC GGGGCTGCCG CAGGCCCAGC TGCTCTGGCG CAAGGTGCCA CTGGACGAGC 980
GCATCGTCTT CTCGGGGAAC CTCTTCCAGC ACCAGGAGGA CAGCAAGAAG TGGAGAAACC GCTTCAGCCT 1050
CGTGCCCCAC AACTACGGGC TGGTGCTCTA CGAAAACAAA GCGGCCTATG AGCGGCAGGT CCCACCACGA 1120
GCCGTCATCA ACAGTCAGG CTACAAAATC CTCACGTCCG TGGACCAATA CCTGGAGCTC ATTGGCAACT 1190
CCTTACCAGG GACCACGGCA AAGTCGGGCA GTGCCCCCAT CCTCAAGTGC CCCACACAGT TCCCGCTCAT 1260
CCTCTGGCAT CCTTATGCGC GTCACTACTA CTTCTGCATG ATGACAGAAG CCGAGCAGGA CAAGTGGCAG 1330
GCTGTGCTGC AGGACTGCAT CCGGCACTGC AACAATGGAA TCCCTGAGGA CTCCAAGGTA GAGGGCCCTG 1400
CGTTCACAGA TGCCATCCGC ATGTACCGAC AGTCCAAGGA GCTGTACGGC ACCTGGGAGA TGCTGTGTGG 1470
GAACGAGGTG CAGATCTGA GCAACCTGGT GATGGAGGAG CTGGGCCCTG AGCTGAAGGC AGAGCTCGGC 1540
CCGCGGCTGA AGGGGAAACC GCAGGAGCGG CAGCGGCAGT GGATCCAGAT CTCGGACGCC GTGTACCACA 1610
TGGTGTACGA GCAGGCCAAG GCGCGCTTCG AGGAGGTGCT GTCCAAGGTG CAGCAGGTGC AGCCGGCCAT 1680
GCAGGCCGTC ATCCGAACTG ACATGGACCA AATTATCACC TCCAAGGAGC ACCTTGCCAG CAAGATCCGA 1750
GCCTTCATCC TCCCCAAGGC AGAGGTGTGC GTGCGGAACC ATGTCCAGCC CTACATCCCA TCCATCCTGG 1820
AGGCCCTGAT GGTCCCACCC AGCCAGGGCT TCACTGAGGT GCGAGATGTC TTCTTCAAGG AGGTCACGGA 1890
CATGAACCTG AACGTCATCA ACGAGGGCGG CATTGACAAG CTGGGCGAGT ACATGGAGAA GCTGTCCCGG 1960
CTGGCGTACC ACCCCCTGAA GATGCAGAGC TGCTATGAGA AGATGGAGTC GCTGCGACTG GACGGGCTGC 2030

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AGCAGCGATT TGATGTGTCC AGCACGTCCG TGTTCAGCA GCGAGCCCAG ATCCACATGC GGGAGCAAAT 2100  
 GGACAATGCC GTGTATACGT TCGAGACCCT CCTGCACCAG GAGCTGGGGA AGGGGCCAC CAAGGAGGAG 2170  
 CTGTGCAAGT CCATCCAGCG GGTCTGGAG CGGGTGCTGA AAAAATACGA CTACGACAGC AGCTCTGTGC 2240  
 GGAAGAGGTT CTTCCGGGAG GCGCTGCTGC AGATCAGCAT CCCGTTCTTG CTCAAGAAGC TGGCCCCTAC 2310  
 CTGCAAGTCG GAGCTGCCCC GGTTCAGGA GCTGATCTTC GAGGACTTTG CCAGGTTTCAT CCTGGTGGAA 2380  
 AACACGTACG AGGAGGTGGT GCTGCAGACC GTCATGAAGG ACATCCTGCA GGCTGTGAAG GAGGCCGCGG 2450  
 TGCAGAGGAA GCACAACCTC TACCGGGACA GCATGGTCAT GCACAACAGC GACCCCAACC TGCACCTGCT 2520  
 GGCCGAGGGC GCCCCATCG ACTGGGGCGA GGAGTACAGC AACAGCGGCG GGGGCGGCAG CCCAGCCCC 2590  
 AGCACCCCGG AGTCAGCCAC CCTCTCGAA AAGCGACGGC GCGCCAAGCA GGTGGTCTCT GTGGTCCAGG 2660  
 ATGAGGAGGT GGGGCTGCCC TTTGAGGCTA GCCCTGAGTC ACCACCACCT GCGTCCCCGG ACGGTGTCAC 2730  
 TGAGATCCGA GGCCTGCTGG CCCAAGTCT GCGGCCTGAG AGCCCCCAC CAGCCGGCCC CCTGCTCAAC 2800  
 GGGGCCCCCG CTGGGGAGAG TCCCCAGCCT AAGGCCGCC CCGAGGCCTC CTCGCCGCTT GCCTCAGCCC 2870  
 TCCAGCATCT CCTGCCTGGA AAGGCTGTGG ACCTTGGGCC CCCAAGCCC AGCGACCAGG AGACTGGAGA 2940  
 GCAGGTGTCC AGCCCCAGCA GCCACCCGCG CCTCCACACC ACCACCGAGG ACAGTGCAGG GGTGCAGACT 3010  
 GAGTTCTAGG CCAGTGGGTC CCTGACTGCT GCACATGGCA CAGGCCGTTT CCTTCCGGAC CCAGGCAGGC 3080  
 TCAGCTCTGG GGAGGGCACC CTGGTCTGTG CTTGTGGGT GGAGGCGGG CAGGGCTGTG TGGACCGCC 3150  
 AGGGAGCGGG CCCACCTGAG TCACTTTATT GGGTTCAGTC AACACTTTCT TGCTCCCTGT TTTCTCTTCT 3220  
 GTGGGATGAT CTCAGATGCA GGGGCTGGTT TTGGGGTTT CTTGCTGTG CCAAGGGCTG GACACTGCTG 3290  
 GGGGGCTGGA AAGCCCTCC CTTCTGTGCC TTCTGTGGCC TCCATCCCT CATGGGTGCT GCCATCCTTC 3360  
 CTGGAGAGAG GGAGGTGAAA GCTGGTGTGA GCCAGTGGG TTCCCGCCA CTCACCCAGG AGCTGGCTGG 3430  
 GCCAGGACCG GGAGAGGGAG CACTGCTGCC CTCCTGGCCC TGCTCCTTCC GCAGTTAGGG GTGGACCGAG 3500  
 CCTCGCTTTC CCCACTGTTC TGGAGGAAG GGAAGGAGG GGGTCTTCAG GCTGGAGCCA GGCTGGGGGT 3570  
 GCTGGGTGGA GAGATGAGAT TTAGGGGTG CCTCATGGG TGGGCAGGCC TGGGGTGAAA TGAGAAAGGC 3640  
 CCAGAACGTG CAGGTCTGCG GAGGGGAAGT GTCCTGAGTG AAGGAGGGA CCCATCCTG GGGATGCTGG 3710  
 GAGTGAGTGA GTGAGATGGC TGAGTGAGGG TTATGGGAG CCTGAGGTTT TATGGGCTG TGTATCCCT 3780  
 TCTCCCGGCC CCAGCCTGCC TCCCTCCTGC CCGCCTGGCC CACAGTCTC CCTCTGGTCC CTGTCCCTCT 3850  
 GGTGGTTGGG GATGGAGCGG CAGCAAGGG TGTAATGGG CTGGGTCTG TCTTCTACAG GCCACCCGA 3920  
 GGTCTCAGT GGTGCTTG GGAGCCGAC GGGGCTCCTG AGGGGTACAG GTTGGGTGG CCCTCCCTGA 3990  
 GGGTCTGGG TCAGGCTTG GCCTCTGCTG CCTCTCAGTC ACCAAGTCAC CTCCTCTGA AAATCCAGTC 4060  
 CCTTCTTTGG ATGTCCTTGT GAGTCACTCT GGGCCTGGCT GTCGTCCCTC CTCAGCTTCT TGTTCTGGG 4130  
 ACAAGGTCA AGCCAGGATG GGCCAGGCN TGGGATCCCC CACCCAGGA CCCACAGGC CCCCTCCCT 4200  
 GNTGNTTTC GGGGGCAGG GCAGAAATGG ACTCCTTTT GGTCCCCGAG GTGGGGTCCC CTCCCAGCCC 4270  
 TGCATCCTCC GTGCCCTAGA CCTGCTCCCC AGAGGAGGGG CTTGACCCA CAGGAAGTGT GGTGGCGCCT 4340  
 GGCAATCAGG GACCCCAAGC TGCCGAGCC CTGGTTTTT GCGCATCTTT TCCCTCTGT CCCGAAGATT 4410

TGCGCCTTTA GTGCCTTTTG AGGGGTCCC ATCATCCCTC CCTGATATTG TATGAAAAT ATTATGCACA 4480  
CTGTCATGC TTTTACTAAT CAATAACGC TTTATTTAAA AAAAAAAAAA AAA 4533

**Figur 4 – Human STR\_50E1 – SEQ ID NO:4**Predicted polypeptide of short splice variant

MEEVGGRWWG LKPRLAGLRG TGSDCPALAQ QQTALKDVLG VRNWASSGPF LLGLSLWRMG WMGEKTKGIL 70  
TEFLQFYEDQ YGVALFNSMR HEIEGTGLPQ AQLLWRKVPL DERIVFSGNL FQHQEDSKKW RNRFSLVPHN 140  
YGLVLYENKA AYERQVPPRA VIN\$AGYKIL TSVDQYLELI GNSLPGTAK SGSAPILKCP TQFPLILWHP 210  
YARHYYFCMM TEAEQDKWQA VLQDCIRHCN NGIPEDSKVE GPAFTDAIRM YRQSKELYGT WEMLCGNEVQ 280  
ILSNLVMEEL GPELKAELGP RLKGKPOERQ ROWIQISDAV YHMVYEQAKA RFEEVLSKVQ QVQPAMQAVI 350  
RTDMDQIITS KEHLASKIRA FILPKAEVCV RNHVOPYIPS ILEALMVPTS QGFTEVRDVF FKEVTDMLN 420  
VINEGGIDKL GEYMEKLSRL AYHPLKMQSC YEKMESLRID GLQQRFDVSS TSVFKQRAQI HMREQMDNAV 490  
YTFETLLHQE LGKGPTKEEL CKSIQVLER VLKKYDYDSS SVRKRFFREA LLQISIPFL KKLAPTCKSE 560  
LPRFQELIFE DFARFILVEN TYEEVVLQTV MKDILQAVKE AAVORKHNLY RDSMVMHNSD PNLHLLAEGA 630  
PIDWGEEYSN SGGGGSPPSPS TPESATLSEK RRRAKQVVS VQDEEVGLPF EASPESPPPA SPDGVTEIRG 700  
LLAQGLRPES PPPAGPLLNG APAGESPOPK AAPEASSPPA SPLQHLPGK AVDLGPPKPS DQETGEQVSS 770  
PSSHPALHTT TEDSAGVQTE F 791